

SEQUENCE LISTING

<110> UEMURA, Hidetoshi
 OKUI, Akira
 KOMINAMI, Katsuya
 YAMAGUCHI, Nozomi
 MITSUI, Shinichi

<120> NOVEL SERINE PROTEASE BSSP4

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 <141> 2001-05-21

<150> JP 10/347813
 <151> 1998-11-20

<150> PCT/JP99/06472
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<170> PatentIn version 3.1

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 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu
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 Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn
 -30 -25 -20

gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg 144
 Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu
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aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg 192
 Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp
 -1 1 5 10

atc gtg agc atc cag aag aat ggg acc cac cac tgc gca ggt tct ctg 240
 Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu

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ctc acc agc cgc tgg gtg atc act gct gcc cac tgt ttc aag gac aac				288
Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn				
	35	40	45	
ctg aac aaa cca tac ctg ttc tct gtg ctg ctg ggg gcc tgg cag ctg				336
Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu				
	50	55	60	
ggg aac cct ggc tct cgg tcc cag aag gtg ggt gtt gcc tgg gtg gag				384
Gly Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu				
	65	70	75	
ccc cac cct gtg tat tcc tgg aag gaa ggt gcc tgt gca gac att gcc				432
Pro His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala				
	80	85	90	
ctg gtg cgt ctc gag cgc tcc ata cag ttc tca gag cgg gtc ctg ccc				480
Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro				
	95	100	105	110
atc tgc cta cct gat gcc tct atc cac ctc cct cca aac acc cac tgc				528
Ile Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys				
	115	120	125	
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Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His				
	130	135	140	
cct cag acc ctg cag aag ctg aag gtt cct atc atc gac tcg gaa gtc				624
Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val				
	145	150	155	
tgc agc cat ctg tac tgg cgg gga gca gga cag gga ccc atc act gag				672
Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu				
	160	165	170	
gac atg ctg tgt gcc ggc tac ttg gag ggg gag cgg gat gct tgt ctg				720
Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu				
	175	180	185	190
ggc gac tcc ggg ggc ccc ctc atg tgc cag gtg gac ggc gcc tgg ctg				768
Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu				
	195	200	205	
ctg gcc ggc atc atc agc tgg ggc gag ggc tgt gcc gag cgc aac agg				816
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg				
	210	215	220	
ccc ggg gtc tac atc agc ctc tct gcg cac cgc tcc tgg gtg gag aag				864
Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys				
	225	230	235	
atc gtg caa ggg gtg cag ctc cgc ggg cgc gct cag ggg ggt ggg gcc				912
Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala				
	240	245	250	
ctc agg gca ccg agc cag ggc tct ggg gcc gcc gcg cgc tcc				954
Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser				
	255	260	265	

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tagggcgag cggaacgcgg ggctcggatc tgaaaggcgg ccagatccac atctggatct 1014
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Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala
      -30                -25                -20

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Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
      -15                -10                -5

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Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
-1  1          5          10          15

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Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu
      20                25                30

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Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu
      35                40                45

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Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly
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Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu Pro
      65                70                75

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His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala Leu
      80                85                90                95

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Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile
      100                105                110

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Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys Trp
 115 120 125

Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro
 130 135 140

Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys
 145 150 155

Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp
 160 165 170 175

Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 180 185 190

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu
 195 200 205

Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg Pro
 210 215 220

Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile
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 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu
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gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg	144
Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu	
-15 -10 -5	
aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg	192
Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp	
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Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu	
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Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn	
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ctg aac aaa cca tac ctg ttc tct gtg ctg ctg ggg gcc tgg cag ctg	336
Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu	
50 55 60	
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Gly Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu	
65 70 75	
ccc cac cct gtg tat tcc tgg aag gaa ggt gcc tgt gca gac att gcc	432
Pro His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala	
80 85 90	
ctg gtg cgt ctc gag cgc tcc ata cag ttc tca gag cgg gtc ctg ccc	480
Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro	
95 100 105 110	
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Ile Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys	
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Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His	
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cct cag acc ctg cag aag ctg aag gtt cct atc atc gac tcg gaa gtc	624
Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val	
145 150 155	
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Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu	
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Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu	
175 180 185 190	
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 Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys
 225 230 235

atc gtg caa ggg gtg cag ctc cgc ggg cgc gct cag ggg ggt ggg gcc 912
 Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala
 240 245 250

ctc agg gca ccg agc cag ggc tct ggg gcc cca gcg ctt ttg tgt ata 960
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Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
 -15 -10 -5

Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
 -1 1 5 10 15

Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu
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Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu
 35 40 45

Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly
 50 55 60

Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu Pro
 65 70 75

His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala Leu
 80 85 90 95

Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile
 100 105 110

Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys Trp
 115 120 125

Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro
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Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys
 145 150 155

Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp
 160 165 170 175

Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 180 185 190

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu
 195 200 205

Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg Pro
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Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile
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Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu
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 Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn
 -30 -25 -20

gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg 144
 Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu
 -15 -10 -5

aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg 192
 Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp
 -1 1 5 10

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ctc acc agc cgc tgg gtg atc act gct gcc cac tgt ttc aag gac aac 288
 Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn
 35 40 45

ctg aac aaa cca tac ctg ttc tct gtg ctg ctg ggg gcc tgg cag ctg 336
 Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu
 50 55 60

ggg aac cct ggc tct cgg tcc cag aag gtg ggt gtt gcc tgg gtg gag 384
 Gly Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu
 65 70 75

ccc cac cct gtg tat tcc tgg aag gaa ggt gcc tgt gca gac att gcc 432
 Pro His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala
 80 85 90

ctg gtg cgt ctc gag cgc tcc ata cag ttc tca gag cgg gtc ctg ccc 480
 Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro
 95 100 105 110

atc tgc cta cct gat gcc tct atc cac ctc cct cca aac acc cac tgc 528
 Ile Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys
 115 120 125

tgg atc tca ggc tgg ggg agc atc caa gat gga gtt ccc ttg ccc cac 576
 Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His
 130 135 140

cct cag acc ctg cag aag ctg aag gtt cct atc atc gac tcg gaa gtc 624
 Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val
 145 150 155

tgc agc cat ctg tac tgg cgg gga gca gga cag gga ccc atc act gag 672
 Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu
 160 165 170

gac atg ctg tgt gcc ggc tac ttg gag ggg gag cgg gat gct tgt ctg 720
 Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu
 175 180 185 190

ggc gac tcc ggg ggc ccc ctc atg tgc cag gtg gac ggc gcc tgg ctg 768
 Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
 195 200 205

ctg gcc ggc atc atc agc tgg ggc gag ggc tgt gcc gag cgc aac agg 816
 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg
 210 215 220

ccc ggg gtc tac atc agc ctc tct gcg cac cgc tcc tgg gtg gag aag 864
 Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys
 225 230 235

atc gtg caa ggg gtg cag ctc cgc ggg cgc ccc cgg gcc cca gcg ctt 912
 Ile Val Gln Gly Val Gln Leu Arg Gly Arg Pro Arg Ala Pro Ala Leu
 240 245 250

ttg tgt ata taaatgttaa tgatttttat aggtatttgt aaccctgccc 961
 Leu Cys Ile
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aaaaaaaaaa aaaaaa 1036

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 -30 -25 -20

Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
 -15 -10 -5

Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
 -1 1 5 10 15

Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu
 20 25 30

Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu
 35 40 45

Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly
 50 55 60

Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu Pro
65 70 75

His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala Leu
80 85 90 95

Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile
100 105 110

Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys Trp
115 120 125

Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro
130 135 140

Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys
145 150 155

Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp
160 165 170 175

Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
180 185 190

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu
195 200 205

Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg Pro
210 215 220

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Cys Ile

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    Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu
              -45                -40                -35

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ggc acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat      96
Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn
              -30                -25                -20

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gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg      144
Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu
              -15                -10                -5

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aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg      192
Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp
    -1  1                5                10

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atc gtg agc atc cag aag aat ggg acc cac cac tgc gca gga caa cct      240
Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Gln Pro
    15                20                25                30

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gaa caa acc ata cct gtt ctc tgt gct gct ggg ggc ctg gca gct ggg      288
Glu Gln Thr Ile Pro Val Leu Cys Ala Ala Gly Gly Leu Ala Ala Gly
              35                40                45

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gaa ccc tgg ctc tcg gtc cca gaa ggt ggg tgt tgc ctg ggt gga gcc      336
Glu Pro Trp Leu Ser Val Pro Glu Gly Gly Cys Cys Leu Gly Gly Ala
              50                55                60

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cca ccc tgt gta ttc ctg gaa gga agg tgc ctg tgc aga cat tgc cct      384
Pro Pro Cys Val Phe Leu Glu Gly Arg Cys Leu Cys Arg His Cys Pro
              65                70                75

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ggt gcg tct cga gcg ctc cat aca gtt ctc aga gcg ggt cct gcc cat      432
Gly Ala Ser Arg Ala Leu His Thr Val Leu Arg Ala Gly Pro Ala His
    80                85                90

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ctg cct acc tgatgcctct tccacctccc tccaaacacc cactgctgga      481
Leu Pro Thr
    95

```

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tctcaggctg ggggagcatc caagatggag ttcccttgcc ccaccctcag accctgcaga      541

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agctgaaggt tcctatcatc gactcggaag tctgcagcca tctgtactgg cggggagcag      601

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gacagggacc catcactgag gacatgctgt gtgccggcta cttggagggg gagcgggatg      661

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cttgtctggg cgactccggg ggccccctca tgtgccaggt ggacggcgcc tggctgctgg      721

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Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
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Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala
      -30                      -25                      -20

```

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Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
      -15                      -10                      -5

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Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
-1  1          5          10          15

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Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Gln Pro Glu
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Gln Thr Ile Pro Val Leu Cys Ala Ala Gly Gly Leu Ala Ala Gly Glu
      35          40          45

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Pro Trp Leu Ser Val Pro Glu Gly Gly Cys Cys Leu Gly Gly Ala Pro
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Pro Cys Val Phe Leu Glu Gly Arg Cys Leu Cys Arg His Cys Pro Gly
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Ala Ser Arg Ala Leu His Thr Val Leu Arg Ala Gly Pro Ala His Leu
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Pro Thr

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ggc acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat 96
 Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn
 -30 -25 -20

gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg 144
 Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu
 -15 -10 -5

aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg 192
 Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp
 -1 1 5 10

atc gtg agc atc cag aag aat ggg acc cac cac tgc gca gtt ccc ttg 240
 Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Val Pro Leu
 15 20 25 30

ccc cac cct cag acc ctg cag aag ctg aag gtt cct atc atc gac tcg 288
 Pro His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser
 35 40 45

gaa gtc tgc agc cat ctg tac tgg cgg gga gca gga cag gga ccc atc 336
 Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile
 50 55 60

act gag gac atg ctg tgt gcc ggc tac ttg gag ggg gag cgg gat gct 384
 Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala
 65 70 75

tgt ctg ggc gac tcc ggg ggc ccc ctc atg tgc cag gtg gac ggc gcc 432
 Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala
 80 85 90

tgg ctg ctg gcc ggc atc atc agc tgg ggc gag ggc tgt gcc gag cgc 480
 Trp Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg
 95 100 105 110

aac agg ccc ggg gtc tac atc agc ctc tct gcg cac cgc tcc tgg gtg 528
 Asn Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val

115	120	125	
gag aag atc gtg caa ggg gtg cag ctc cgc ggg cgc gct cag ggg ggt			576
Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly			
130	135	140	
ggg gcc ctc agg gca ccg agc cag ggc tct ggg gcc gcc gcg cgc tcc			624
Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser			
145	150	155	
tagggcgag cgggacgcgg ggctcggatc tgaaaggcgg ccagatccac atctggatct			684
ggatctgcgg cggcctcggg cggtttcccc cgccgtaaat aggctcatct acctctacct			744
ctggggggccc ggacggctgc tgcggaaagg aaacccccctc cccgaccgc cgcacggcct			804
caggccccgc cctccaaggc atcaggcccc gcccaacggc ctcatgtccc cgccccacg			864
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Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala			
-30	-25	-20	
Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn			
-15	-10	-5	
Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile			
-1 1	5	10	15
Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Val Pro Leu Pro			
20	25	30	
His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu			
35	40	45	
Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr			
50	55	60	
Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys			
65	70	75	

Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp
80 85 90 95

Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
100 105 110

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu
115 120 125

Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly
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Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser
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<211> 1083
<212> DNA
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Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn
-30 -25 -20

gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg 144
Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu
-15 -10 -5

aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg 192
Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp
-1 1 5 10

atc gtg agc atc cag aag aat ggg acc cac cac tgc gca ggt tct ctg 240
Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu
15 20 25 30

ctc acc agc cgc tgg gtg atc act gct gcc cac tgt ttc aag gac aac 288
Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn

35	40	45	
ctg aac aaa cca tac ctg ttc tct	gtg ctg ctg ggg gcc tgg cag ctg		336
Leu Asn Lys Pro Tyr Leu Phe Ser	Val Leu Leu Gly Ala Trp Gln Leu		
50	55	60	
ggg aac cct ggc tct cgg tcc cag aag ttc cct tgc ccc acc ctc aga			384
Gly Asn Pro Gly Ser Arg Ser Gln Lys Phe Pro Cys Pro Thr Leu Arg			
65	70	75	
ccc tgc aga agc tgaaggttcc tatcatcgac tcggaagtct gcagccatct			436
Pro Cys Arg Ser			
80			
gtactggcgg ggagcaggac agggaccccat cactgaggac atgctgtgtg ccggctactt			496
ggaggggggag cgggatgctt gtctgggcga ctccgggggc cccctcatgt gccaggtgga			556
cgggcgcttg ctgctggccg gcatcatcag ctggggcgag ggctgtgccg agcgcaacag			616
gcccggggtc tacatcagcc tctctgcgca ccgctcctgg gtggagaaga tcgtgcaagg			676
ggtgcagctc cgcgggcgcg ctcagggggg tggggccctc agggcaccga gccagggctc			736
tggggccgcc gcgcgctcct agggcgcgagc gggacgcggg gctcggatct gaaaggcggc			796
cagateccaca tctggatctg gatctgcggc ggccctcgggc ggtttccccc gccgtaaata			856
ggctcatcta cctctacctc tgggggcccc gacggctgct gcggaaagga aaccccctcc			916
ccgaccgcc cgacggcctc agggccccgcc ctccaaggca tcaggccccg cccaacggcc			976
tcatgtcccc gccccacga cttccggccc cgccccggg cccagcgct tttgtgtata			1036
taaatgttaa tgatttttat aggtatttgt aaccctgccc acatata			1083
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-30	-25	-20	
Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn			
-15	-10	-5	
Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile			
-1 1	5	10	15
Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu			

20

25

30

Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu
 35 40 45

Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly
 50 55 60

Asn Pro Gly Ser Arg Ser Gln Lys Phe Pro Cys Pro Thr Leu Arg Pro
 65 70 75

Cys Arg Ser
 80

<210> 13
 <211> 723
 <212> DNA
 <213> Homo sapiens

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 <222> (4)..(705)
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<400> 13
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 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu
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ggc acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat 96
 Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn
 -30 -25 -20

gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg 144
 Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu
 -15 -10 -5

aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg 192
 Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp
 -1 1 5 10

atc gtg agc atc cag aag aat ggg acc cac cac tgc gca ggt tct ctg 240
 Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu
 15 20 25 30

ctc acc agc cgc tgg gtg atc act gct gcc cac tgt ttc aag gac aac 288
 Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn
 35 40 45

ctg aac aaa cca tac ctg ttc tct gtg ctg ctg ggg gcc tgg cag ctg 336
 Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu
 50 55 60

ggg aac cct ggc tct cgg tcc cag aag gtg ggt gtt gcc tgg gtg gag 384
 Gly Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu
 65 70 75

ccc cac cct gtg tat tcc tgg aag gaa ggt gcc tgt gca gac att gcc 432
 Pro His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala
 80 85 90

ctg gtg cgt ctc gag cgc tcc ata cag ttc tca gag cgg gtc ctg ccc 480
 Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro
 95 100 105 110

atc tgc cta cct gat gcc tct atc cac ctc cct cca aac acc cac tgc 528
 Ile Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys
 115 120 125

tgg atc tca ggc tgg ggg agc atc caa gat gga gtt ccc ttg ccc cac 576
 Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His
 130 135 140

cct cag acc ctc tcc aag gca tca ggc ccc gcc caa cgg cct cat gtc 624
 Pro Gln Thr Leu Ser Lys Ala Ser Gly Pro Ala Gln Arg Pro His Val
 145 150 155

ccc gcc ccc acg act tcc ggc ccc gcc ccg ggc ccc agc gct ttt gtg 672
 Pro Ala Pro Thr Thr Ser Gly Pro Ala Pro Gly Pro Ser Ala Phe Val
 160 165 170

tat ata aat gtt aat gat ttt tat agg tat ttg taaccctgcc cacatata 723
 Tyr Ile Asn Val Asn Asp Phe Tyr Arg Tyr Leu
 175 180 185

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 <211> 234
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 <213> Homo sapiens

<400> 14

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
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Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala
 -30 -25 -20

Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
 -15 -10 -5

Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
 -1 1 5 10 15

Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu

	20		25		30										
Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Lys	Asp	Asn	Leu
			35					40					45		
Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	Leu	Gly	Ala	Trp	Gln	Leu	Gly
		50					55					60			
Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	Val	Gly	Val	Ala	Trp	Val	Glu	Pro
	65					70					75				
His	Pro	Val	Tyr	Ser	Trp	Lys	Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu
80					85					90				95	
Val	Arg	Leu	Glu	Arg	Ser	Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile
				100					105					110	
Cys	Leu	Pro	Asp	Ala	Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp
			115					120					125		
Ile	Ser	Gly	Trp	Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro
		130					135					140			
Gln	Thr	Leu	Ser	Lys	Ala	Ser	Gly	Pro	Ala	Gln	Arg	Pro	His	Val	Pro
	145					150					155				
Ala	Pro	Thr	Thr	Ser	Gly	Pro	Ala	Pro	Gly	Pro	Ser	Ala	Phe	Val	Tyr
160					165					170					175
Ile	Asn	Val	Asn	Asp	Phe	Tyr	Arg	Tyr	Leu						
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<210> 15
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 <223>

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 <221> mat_peptide
 <222> (151)..()
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<400> 15

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gcc atg gtg gtt tct gga gcg ccc cca gcc ctg ggt ggg ggc tgt ctg      48
  Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu
                                -45                                -40                                -35

ggc acc ttc*acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctg aat      96
Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn
                                -30                                -25                                -20

gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg     144
Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu
                                -15                                -10                                -5

aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg     192
Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp
    -1  1                                5                                10

atc gtg agc atc cag aag aat ggg acc cac cac tgc gca ggt tct ctg     240
Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu
    15                                20                                25                                30

ctc acc agc cgc tgg gtg atc act gct gcc cac tgt ttc aag gat tcc     288
Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Ser
                                35                                40                                45

ctt gcc cca ccc tca gac cct gca gaa gct gaa ggt tcc tat cat cga     336
Leu Ala Pro Pro Ser Asp Pro Ala Glu Ala Glu Gly Ser Tyr His Arg
                                50                                55                                60

ctc gga agt ctg cag cca tct gta ctg gcg ggg agc agg aca ggg acc     384
Leu Gly Ser Leu Gln Pro Ser Val Leu Ala Gly Ser Arg Thr Gly Thr
    65                                70                                75

cat cac tgaggacatg ctgtgtgccg gctacttgga gggggagcgg gatgcttgct     440
His His
    80

tgggcgactc cgggggcccc ctcatgtgcc aggtggacgg cgccctggctg ctggccggca     500

tcatcagctg gggcgagggc tgtgccgagc gcaacaggcc cggggtctac atcagcctct     560

ctgcgcaccg ctctgggtg gagaagatcg tgcaaggggt gcagctccgc gggcgcgctc     620

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ctgcggcggc ctcgggcggt ttccccgcgc gtaaataaggc tcatctacct ctacctctgg     800

gggcccggac ggctgctgcg gaaaggaaac cccctccccg acccgcccga cgccctcagg     860

ccccgccctc caaggcatca ggccccgcgc aacggcctca tgtccccgcgc ccacgactt     920

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<210> 16
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<212> PRT
<213> Homo sapiens

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<400> 16

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 -30 -25 -20

Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
 -15 -10 -5

Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
 -1 1 .5 10 15

Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu
 20 25 30

Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Ser Leu
 35 40 45

Ala Pro Pro Ser Asp Pro Ala Glu Ala Glu Gly Ser Tyr His Arg Leu
 50 55 60

Gly Ser Leu Gln Pro Ser Val Leu Ala Gly Ser Arg Thr Gly Thr His
 65 70 75

His
 80

<210> 17
 <211> 948
 <212> DNA
 <213> Homo sapiens

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 <222> (4)..(909)
 <223>

<220>
 <221> mat_peptide
 <222> (151)..()
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<400> 17

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 -45 -40 -35

48

ggc acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat	96
Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn	
-30 -25 -20	
gcg gcc agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg	144
Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu	
-15 -10 -5	
aac cgg gtt gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg	192
Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp	
-1 1 5 10	
atc gtg agc atc cag aag aat ggg acc cac cac tgc gca ggt tct ctg	240
Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu	
15 20 25 30	
ctc acc agc cgc tgg gtg atc act gct gcc cac tgt ttc aag gac aac	288
Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn	
35 40 45	
ctg aac aaa cca tac ctg ttc tct gtg ctg ctg ggg gcc tgg cag ctg	336
Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu	
50 55 60	
ggg aac cct ggc tct cgg tcc cag aaa gtg ggt gtt gcc tgg gtg gag	384
Gly Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu	
65 70 75	
ccc cac cct gtg tat tcc tgg aag gaa ggt gcc tgt gca gac att gcc	432
Pro His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala	
80 85 90	
ctg gtg cgt ctc gag cgc tcc ata cag ttc tca gag cgg gtc ctg ccc	480
Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro	
95 100 105 110	
atc tgc cta cct gat gcc tct atc cac ctc cct cca aac acc cac tgc	528
Ile Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys	
115 120 125	
tgg atc tca ggc tgg ggg agc atc caa gat gga gtt ccc ttg ccc cac	576
Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His	
130 135 140	
cct cag acc ctg cag aag ctg aag gtt cct atc atc gac tcg gaa gtc	624
Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val	
145 150 155	
tgc agc cat ctg tac tgg cgg gga gca gga cag gga ccc atc act gag	672
Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu	
160 165 170	
gac atg ctg tgt gcc ggc tac ttg gag ggg gag cgg gat gct tgt ctg	720
Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu	
175 180 185 190	
gtg agc tcc ctc gag ccc ccc acc cct ggc cag gag ggc ctc ggg aag	768
Val Ser Ser Leu Glu Pro Pro Thr Pro Gly Gln Glu Gly Leu Gly Lys	
195 200 205	
gag cca gcg tca gtc ctg tcc cca ctg agc ccc aca acc tct ccc tgg	816

Glu Pro Ala Ser Val Leu Ser Pro Leu Ser Pro Thr Thr Ser Pro Trp
 210 215 220
 cct cct ccc cag aac tgg ctg tgc ctg aca gtc ccg ggt ccc cat aga 864
 Pro Pro Pro Gln Asn Trp Leu Cys Leu Thr Val Pro Gly Pro His Arg
 225 230 235
 acc agc ctc agc ctg gct cag cca ctc act tat ttg ttc aga cat 909
 Thr Ser Leu Ser Leu Ala Gln Pro Leu Thr Tyr Leu Phe Arg His
 240 245 250
 taaactgggc atcccagctg caaaaaaaaaa aaaaaaaaaa 948

 <210> 18
 <211> 302
 <212> PRT
 <213> Homo sapiens

 <400> 18
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 -30 -25 -20
 Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
 -15 -10 -5
 Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
 -1 1 5 10 15
 Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu
 20 25 30
 Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu
 35 40 45
 Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly
 50 55 60
 Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu Pro
 65 70 75
 His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala Leu
 80 85 90 95
 Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile
 100 105 110

Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys Trp
 115 120 125

Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro
 130 135 140

Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys
 145 150 155

Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp
 160 165 170 175

Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Val
 180 185 190

Ser Ser Leu Glu Pro Pro Thr Pro Gly Gln Glu Gly Leu Gly Lys Glu
 195 200 205

Pro Ala Ser Val Leu Ser Pro Leu Ser Pro Thr Thr Ser Pro Trp Pro
 210 215 220

Pro Pro Gln Asn Trp Leu Cys Leu Thr Val Pro Gly Pro His Arg Thr
 225 230 235

Ser Leu Ser Leu Ala Gln Pro Leu Thr Tyr Leu Phe Arg His
 240 245 250

<210> 19
 <211> 1322
 <212> DNA
 <213> Mus. Sp.

<220>
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<220>
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 gtctccaccc ataccagca atg atg atc tcc aga cct ccc cca gca ctg ggt 112
 Met Met Ile Ser Arg Pro Pro Pro Ala Leu Gly
 -45 -40
 ggg gac cag ttc agc atc tta atc ctt ctg gtg ctg ctg act tcc aca 160

Gly	Asp	Gln	Phe	Ser	Ile	Leu	Ile	Leu	Leu	Val	Leu	Leu	Thr	Ser	Thr		
			-35					-30					-25				
gct	ccc	atc	agt	gct	gcc	acc	atc	cga	gtg	tcc	cca	gac	tgt	ggg	aag	208	
Ala	Pro	Ile	Ser	Ala	Ala	Thr	Ile	Arg	Val	Ser	Pro	Asp	Cys	Gly	Lys		
		-20					-15				-10						
cct	cag	cag	ctg	aac	cgg	att	gtg	gga	ggg	gag	gac	agc	atg	gat	gcc	256	
Pro	Gln	Gln	Leu	Asn	Arg	Ile	Val	Gly	Gly	Glu	Asp	Ser	Met	Asp	Ala		
	-5				-1	1				5					10		
cag	tgg	ccc	tgg	att	gtt	agc	atc	ctc	aag	aat	ggc	tcc	cac	cac	tgt	304	
Gln	Trp	Pro	Trp	Ile	Val	Ser	Ile	Leu	Lys	Asn	Gly	Ser	His	His	Cys		
			15					20						25			
gca	ggc	tcc	ctg	ctc	acc	aac	cgc	tgg	gtg	gtc	aca	gcc	gcg	cac	tgc	352	
Ala	Gly	Ser	Leu	Leu	Thr	Asn	Arg	Trp	Val	Val	Thr	Ala	Ala	His	Cys		
			30					35					40				
ttt	aag	agc	aat	atg	gac	aaa	cca	tct	ctg	ttc	tca	gta	ttg	ttg	ggg	400	
Phe	Lys	Ser	Asn	Met	Asp	Lys	Pro	Ser	Leu	Phe	Ser	Val	Leu	Leu	Gly		
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gcc	tgg	aag	ctg	ggg	agc	cca	ggc	cca	agg	tcc	cag	aaa	gta	ggc	att	448	
Ala	Trp	Lys	Leu	Gly	Ser	Pro	Gly	Pro	Arg	Ser	Gln	Lys	Val	Gly	Ile		
	60					65					70						
gct	tgg	gtg	ctg	cct	cac	ccc	agg	tat	tct	tgg	aag	gag	gga	acc	cat	496	
Ala	Trp	Val	Leu	Pro	His	Pro	Arg	Tyr	Ser	Trp	Lys	Glu	Gly	Thr	His		
75					80					85					90		
gca	gac	att	gcc	ctg	gtg	cgc	ctg	gaa	cac	tcc	atc	cag	ttc	tct	gag	544	
Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	His	Ser	Ile	Gln	Phe	Ser	Glu		
				95					100						105		
cgg	atc	ctg	ccc	atc	tgc	cta	cct	gac	tcc	tct	gtc	cgt	ctc	cct	ccc	592	
Arg	Ile	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ser	Ser	Val	Arg	Leu	Pro	Pro		
			110					115					120				
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Lys	Thr	Asp	Cys	Trp	Ile	Ala	Gly	Trp	Gly	Ser	Ile	Gln	Asp	Gly	Val		
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ccc	ctg	ccc	cac	cct	cag	acc	ctt	cag	aag	ctg	aag	gtg	ccc	atc	atc	688	
Pro	Leu	Pro	His	Pro	Gln	Thr	Leu	Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile		
		140					145				150						
gac	tcc	gaa	ctc	tgc	aaa	agc	ttg	tac	tgg	cgg	gga	gcc	ggg	cag	gaa	736	
Asp	Ser	Glu	Leu	Cys	Lys	Ser	Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Glu		
		155			160				165						170		
gcc	atc	acg	gag	ggc	atg	ctg	tgt	gct	ggg	tac	ctg	gaa	ggg	gag	cgg	784	
Ala	Ile	Thr	Glu	Gly	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg		
				175					180						185		
gat	gct	tgt	ctg	ggc	gac	tct	ggg	ggg	ccc	ctg	atg	tgc	cag	gtg	gat	832	
Asp	Ala	Cys	Leu	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp		
			190					195					200				
gac	cac	tgg	cta	ctg	act	ggc	ata	atc	agc	tgg	gga	gag	ggc	tgc	gga	880	
Asp	His	Trp	Leu	Leu	Thr	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Gly		

26

65		70		75
His Pro Arg Tyr Ser Trp Lys Glu Gly Thr His Ala Asp Ile Ala Leu				
80		85		90 95
Val Arg Leu Glu His Ser Ile Gln Phe Ser Glu Arg Ile Leu Pro Ile				
	100		105	110
Cys Leu Pro Asp Ser Ser Val Arg Leu Pro Pro Lys Thr Asp Cys Trp				
	115		120	125
Ile Ala Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro				
	130		135	140
Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Leu Cys				
	145		150	155
Lys Ser Leu Tyr Trp Arg Gly Ala Gly Gln Glu Ala Ile Thr Glu Gly				
	160		165	170 175
Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly				
	180		185	190
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Asp His Trp Leu Leu				
	195		200	205
Thr Gly Ile Ile Ser Trp Gly Glu Gly Cys Gly Ala Gln Pro Ala Arg				
	210		215	220
Cys Val His Gln Pro Pro Ser Ser Pro Leu Leu Gly Ala Lys Asp Arg				
	225		230	235
Ser Arg Gly Ala Ala Ala Arg Val Leu Gly Gly Gln Trp Gly His Arg				
	240		245	250 255
Lys Leu Leu Ile				

<210> 21

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 21

aagcttggct agcaacacca tgaatctact cctgatacctt acctttgttg ctgctgctgt

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tgctgcccc tttgacgacg atgacaagga tccgaattc

99

<210> 22
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 22
 gaattcggat ccttgatcatc gtcgtcaaag ggggcagcaa cagcagcagc aacaaaggta 60

aggatcagga gtagattcat ggtgttgcta gccaaagctt 99

<210> 23
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

<400> 23
 ttggtgcatg gcgga 15

<210> 24
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

<400> 24
 tcctcgagac ttggcctgaa tggtttt 27

<210> 25
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid pSecTrypHis/Neurosin

<400> 25
 gcgctagcag atctccatga atctactcct gatcc 35

<210> 26
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p
 SecTrypHis/Neurosin

<400> 26
 tgaagcttgc catggaccaa cttgtcatc 29

<210> 27
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p
 TrypHis

<400> 27
 ccaagcttca ccatcaccat caccat 26

<210> 28
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p
 TrypSigTag

<400> 28
 gcacagtcga ggctgat 17

<210> 29
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify a portion of plasmid p
 FBTrypSigTag

<400> 29
 caaatgtggt atggctg 17

<210> 30
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify conserved region of se
 rin proteases-encoding sequence

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> n is a, c, g or t.

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> n is a, c, g or t.

<400> 30
 gtgctcacng cngcbcaytg

20

<210> 31
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify conserved region of se
 rin proteases-encoding sequence

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> n is a, c, g or t.

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> n is a, c, g or t.

<400> 31
 ccvctrwsdc cncnnggcga

20

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as hBSSP4F1 for RACE f
 or human BSSP4 (forward)

<400> 32
 aggttcctat catcgactcg

20

<210> 33
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer designated as hBSSP4F2 for RACE f
 or human BSSP4 (forward)

<400> 33
 tgaggacatg ctgtgtgccg g

21

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP4F3 to amplify mature human BSSP4-encoding region (forward)

 <400> 34
 gttgtgggcg gcgaggacag 20

 <210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP4F6 to amplify full-length human BSSP4-encoding mRNA (forward)

 <400> 35
 gccatggtgg tttctggagc 20

 <210> 36
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP4R1 for RACE for human BSSP4 (reverse)

 <400> 36
 tatggtttgc tcaggttgct c 21

 <210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP4R2 for RACE for human BSSP4 (reverse)

 <400> 37
 agggcaatgt ctgcacaggc 20

 <210> 38
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP4R3/E to amplify

fy full-length human BSSP4-encoding mRNA (reverse)

<400> 38
ctgaattcct aggagcgcgc ggcggcc 27

<210> 39
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP4R4/E to amplify full-length human BSSP4-encoding mRNA (reverse)

<400> 39
gagaattcga tatgtgggca gggttaca 28

<210> 40
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 40
acaaaccatc tctgttctca g 21

<210> 41
<211> 20
<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as mBSSP4F2 for RACE forward or mouse BSSP4 (forward)

<400> 41
gtcccagaaa gtaggcattg 20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP4F3 to amplify full-length mouse BSSP4-encoding mRNA (forward)

<400> 42
ctccacccat accagcaatg 20

<210> 43
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP4F4 to amplify mature mouse BSSP4-encoding region (forward)

<400> 43

attgtgggag gtgaggacag 20

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP4.2 for RACE f or mouse BSSP4 (reverse)

<400> 44

tgcagagttc ggagtcgatg 20

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP4R2 for RACE f or mouse BSSP4 (reverse)

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<210> 46

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP4R3/P to amplify full-length mouse BSSP4-encoding mRNA (reverse)

<400> 46

attctgcagt tccttggttct ctcgctcagg 30

<210> 47

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 47

aagcttggct agcaacacca tgaatctact cctgatcctt acctttgttg ctgctgctgt 60

tgctgcccc tttcaccatc accatcacca tgacgacgat gacaaggatc cgaattc 117

<210> 48
 <211> 117
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 48
 gaattcggat ccttgatcatc gtcgtcatgg tgatggatgat ggtgaaaggg ggcagcaaca 60
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<210> 49
 <211> 73
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 49
~~gagcgccttttg~~ agcgccttttg tgtatataaa tgtaaatgat ttttataggt atttgtaacc 60

<211> 11
 <212> PRT 73
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<220>
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<400> 50

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 1 5 10

<210> 51
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 51

Asp Asp Asp Asp Lys
 1 5

<210> 52
 <211> 4
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 52

Leu Val His Gly

1

SEQUENCE LISTING

5 <110> Fuso Pharmaceutical Industries Ltd.

 <120> Novel serine protease BSSP4

 <130> 661639

10 <150> JP 10-347813

 <151> 1998-11-20

 <160> 48

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 <212> DNA

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	agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt 153			
	Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val			
	-15	-10	-5	-1 1
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	Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile			
	5	10	15	
	cag aag aat ggg acc cac cac tgc gca ggt tct ctg ctc acc agc cgc tgg 255			
	Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp			
10	20	25	30	35
	gtg atc act gct gcc cac tgt ttc aag gac aac ctg aac aaa cca tac ctg 306			
	Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu			
	40	45	50	
	ttc tct gtg ctg ctg ggg gcc tgg cag ctg ggg aac cct ggc tct cgg tcc 357			
15	Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser			
	55	60	65	
	cag aag gtg ggt gtt gcc tgg gtg gag ccc cac cct gtg tat tcc tgg aag 408			
	Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys			
	70	75	80	85
20	gaa ggt gcc tgt gca gac att gcc ctg gtg cgt ctc gag cgc tcc ata cag 459			
	Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln			
	90	95	100	
	ttc tca gag cgg gtc ctg ccc atc tgc cta cct gat gcc tct atc cac ctc 510			
	Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu			
25	105	110	115	120

cct cca aac acc cac tgc tgg atc tca ggc tgg ggg agc atc caa gat gga 561
 Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly
 125 130 135
 gtt ccc ttg ccc cac cct cag acc ctg cag aag ctg aag gtt cct atc atc 612
 5 Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile
 140 145 150
 gac tcg gaa gtc tgc agc cat ctg tac tgg cgg gga gca gga cag gga ccc 663
 Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro
 155 160 165 170
 10 atc act gag gac atg ctg tgt gcc ggc tac ttg gag ggg gag cgg gat gct 714
 Ile Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala
 175 180 185
 tgt ctg ggc gac tcc ggg ggc ccc ctc atg tgc cag gtg gac ggc gcc tgg 765
 Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp
 15 190 195 200 205
 ctg ctg gcc ggc atc atc agc tgg ggc gag ggc tgt gcc gag cgc aac agg 816
 Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg
 210 215 220
 ccc ggg gtc tac atc agc ctc tct gcg cac cgc tcc tgg gtg gag aag atc 867
 20 Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile
 225 230 235
 gtg caa ggg gtg cag ctc cgc ggg cgc gct cag ggg ggt ggg gcc ctc agg 918
 Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu Arg
 240 245 250 255
 25 gca ccg agc cag ggc tct ggg gcc gcc gcg cgc tcc tagggcgag cgggacgcgg974

Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser

260

265

ggctcggatc tgaaaggcgg ccagatccac atctggatct ggatctgcgg cggcctcggg 1034
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 5 tgcggaaagg aaacccctc cccgaccgc cgcacggcct caggccccgc cctccaaggc 1154
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 cacatata 1282

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 <211> 317
 <212> PRT
 <213> human

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20 -30 -25 -20

Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

-15 -10 -5 -1 1

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

5 10 15

25 Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp

	20	25	30	35
	Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu			
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	Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser			
5	55	60	65	
	Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys			
	70	75	80	85
	Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln			
	90	95	100	
10	Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu			
	105	110	115	120
	Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly			
	125	130	135	
	Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile			
15	140	145	150	
	Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro			
	155	160	165	170
	Ile Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala			
	175	180	185	
20	Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp			
	190	195	200	205
	Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg			
	210	215	220	
	Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile			
25	225	230	235	

Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu Arg

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Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser

260 265

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<210> 3

<211> 1007

<212> DNA

<213> human

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Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30 -25 -20

agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt 153

Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

20 -15 -10 -5 -1 1

gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg atc gtg agc atc 204

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

5 10 15

cag aag aat ggg acc cac cac tgc gca ggt tct ctg ctc acc agc cgc tgg 255

25 Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp

	20	25	30	35	
	gtg atc act gct gcc cac tgt ttc aag gac aac ctg aac aaa cca tac ctg	306			
	Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu				
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5	ttc tct gtg ctg ctg ggg gcc tgg cag ctg ggg aac cct ggc tct cgg tcc	357			
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	cag aag gtg ggt gtt gcc tgg gtg gag ccc cac cct gtg tat tcc tgg aag	408			
	Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys				
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	gaa ggt gcc tgt gca gac att gcc ctg gtg cgt ctc gag cgc tcc ata cag	459			
	Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln				
	90	95	100		
	ttc tca gag cgg gtc ctg ccc atc tgc cta cct gat gcc tct atc cac ctc	510			
15	Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu				
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	cct cca aac acc cac tgc tgg atc tca ggc tgg ggg agc atc caa gat gga	561			
	Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly				
	125	130	135		
20	gtt ccc ttg ccc cac cct cag acc ctg cag aag ctg aag gtt cct atc atc	612			
	Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile				
	140	145	150		
	gac tcg gaa gtc tgc agc cat ctg tac tgg cgg gga gca gga cag gga ccc	663			
	Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro				
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 Ile Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala
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 tgt ctg ggc gac tcc ggg ggc ccc ctc atg tgc cag gtg gac ggc gcc tgg 765
 5 Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp
 190 195 200 205
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 Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg
 210 215 220
 10 ccc ggg gtc tac atc agc ctc tct gcg cac cgc tcc tgg gtg gag aag atc 867
 Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile
 225 230 235
 gtg caa ggg gtg cag ctc cgc ggg cgc gct cag ggg ggt ggg gcc ctc agg 918
 Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu Arg
 15 240 245 250 255
 gca ccg agc cag ggc tct ggg gcc cca gcg ctt ttg tgt ata taaatgttaa 970
 Ala Pro Ser Gln Gly Ser Gly Ala Pro Ala Leu Leu Cys Ile
 260 265 270
 tgatttttat aggtatttgt aaccctgccc acatata 1007
 20
 <210> 4
 <211> 319
 <212> PRT
 <213> human

<400> 4

	Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	Gly	
					-45					-40					-35		
	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	Asn	Ala	Ala
5				-30					-25					-20			
	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	Gln	Leu	Asn	Arg	Val
		-15					-10				-5			-1		1	
	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	Trp	Pro	Trp	Ile	Val	Ser	Ile
			5					10					15				
10	Gln	Lys	Asn	Gly	Thr	His	His	Cys	Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp
		20					25					30				35	
	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu
				40					45					50			
	Phe	Ser	Val	Leu	Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser
15			55					60						65			
	Gln	Lys	Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
		70					75				80				85		
	Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	Ile	Gln
			90					95					100				
20	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	Ser	Ile	His	Leu
		105					110				115				120		
	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	Gly	Ser	Ile	Gln	Asp	Gly
				125				130					135				
	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu	Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile
25			140					145					150				

10

Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro

155 160 165 170

Ile Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala

175 180 185

5 Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp

190 195 200 205

Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg

210 215 220

Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile

10 225 230 235

Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu Arg

240 245 250 255

Ala Pro Ser Gln Gly Ser Gly Ala Pro Ala Leu Leu Cys Ile

260 265 270

15

<210> 5

<211> 1036

<212> DNA

<213> human

20

<400> 5

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Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

-45 -40 -35

25 acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat gcg gcc 102

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala
 -30 -25 -20
 agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt 153
 Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val
 5 -15 -10 -5 -1 1
 gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg atc gtg agc atc 204
 Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile
 5 10 15
 cag aag aat ggg acc cac cac tgc gca ggt tct ctg ctc acc agc cgc tgg 255
 10 Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp
 20 25 30 35
 gtg atc act gct gcc cac tgt ttc aag gac aac ctg aac aaa cca tac ctg 306
 Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu
 40 45 50
 15 ttc tct gtg ctg ctg ggg gcc tgg cag ctg ggg aac cct ggc tct cgg tcc 357
 Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser
 55 60 65
 cag aag gtg ggt gtt gcc tgg gtg gag ccc cac cct gtg tat tcc tgg aag 408
 Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys
 20 70 75 80 85
 gaa ggt gcc tgt gca gac att gcc ctg gtg cgt ctc gag cgc tcc ata cag 459
 Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln
 90 95 100
 ttc tca gag cgg gtc ctg ccc atc tgc cta cct gat gcc tct atc cac ctc 510
 25 Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu

	105	110	115	120	
	cct cca aac acc cac tgc tgg atc tca ggc tgg ggg agc atc caa gat gga	561			
	Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly				
	125	130	135		
5	gtt ccc ttg ccc cac cct cag acc ctg cag aag ctg aag gtt cct atc atc	612			
	Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile				
	140	145	150		
	gac tcg gaa gtc tgc agc cat ctg tac tgg cgg gga gca gga cag gga ccc	663			
	Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro				
10	155	160	165	170	
	atc act gag gac atg ctg tgt gcc ggc tac ttg gag ggg gag cgg gat gct	714			
	Ile Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala				
	175	180	185		
	tgt ctg ggc gac tcc ggg ggc ccc ctc atg tgc cag gtg gac ggc gcc tgg	765			
15	Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp				
	190	195	200	205	
	ctg ctg gcc ggc atc atc agc tgg ggc gag ggc tgt gcc gag cgc aac agg	816			
	Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg				
	210	215	220		
20	ccc ggg gtc tac atc agc ctc tct gcg cac cgc tcc tgg gtg gag aag atc	867			
	Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile				
	225	230	235		
	gtg caa ggg gtg cag ctc cgc ggg cgc ccc cgg gcc cca gcg ctt ttg tgt	918			
	Val Gln Gly Val Gln Leu Arg Gly Arg Pro Arg Ala Pro Ala Leu Leu Cys				
25	240	245	250	255	

ata taaatgtaa tgatttttat aggtatttgt aaccctgccc acatatctta 971

Ile

tttattcctc caatttcaat aaattattta ttctccagaa aaaaaaaaaa aaaaaaaaaa 1031

5 aaaaaa 1036

<210> 6

<211> 306

<212> PRT

10 <213> human

<400> 6

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

-45

-40

-35

15 Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30

-25

-20

Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

-15

-10

-5

-1 1

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

20

5

10

15

Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp

20

25

30

35

Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu

40

45

50

25 Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser

55 60 65
 Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys
 70 75 80 85
 Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln
 5 90 95 100
 Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu
 105 110 115 120
 Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly
 125 130 135
 10 Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile
 140 145 150
 Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro
 155 160 165 170
 Ile Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala
 15 175 180 185
 Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp
 190 195 200 205
 Leu Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg
 210 215 220
 20 Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile
 225 230 235
 Val Gln Gly Val Gln Leu Arg Gly Arg Pro Arg Ala Pro Ile Leu Leu Cys
 240 245 250 255
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<210> 7

<211> 1232

<212> DNA

<213> human

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<400> 7

gcc atg gtg gtt tct gga gcg ccc cca gcc ctg ggt ggg ggc tgt ctc ggc 51

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

-45

-40

-35

10 acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat gcg gcc 102

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30

-25

-20

agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt 153

Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

15 -15 -10 -5 -1 1

gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg atc gtg agc atc 204

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

5

10

15

cag aag aat ggg acc cac cac tgc gca gga caa cct gaa caa acc ata cct 255

20 Gln Lys Asn Gly Thr His His Cys Ala Gly Gln Pro Glu Gln Thr Ile Pro

20

25

30

35

gtt ctc tgt gct gct ggg ggc ctg gca gct ggg gaa ccc tgg ctc tcg gtc 306

Val Leu Cys Ala Ala Gly Gly Leu Ala Ala Gly Glu Pro Trp Leu Ser Val

40

45

50

25 cca gaa ggt ggg tgt tgc ctg ggt gga gcc cca ccc tgt gta ttc ctg gaa 357

Pro Glu Gly Gly Cys Cys Leu Gly Gly Ala Pro Pro Cys Val Phe Leu Glu

55

60

65

gga agg tgc ctg tgc aga cat tgc cct ggt gcg tct cga gcg ctc cat aca 408

Gly Arg Cys Leu Cys Arg His Cys Pro Gly Ala Ser Arg Ala Leu His Thr

5

70

75

80

85

gtt ctc aga gcg ggt cct gcc cat ctg cct acc tgatgcctct atccacctcc 461

Val Leu Arg Ala Gly Pro Ala His Leu Pro Thr

90

95

ctccaaacac ccactgctgg atctcaggct gggggagcat ccaagatgga gttcccttgc 521

10

cccacctca gacctgcag aagctgaagg ttctatcat cgactcgaa gtctgcagcc 581

atctgtactg gcggggagca ggacaggac ccatcactga ggacatgtg tgtgccggct 641

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tggacggcgc ctggctgtg gccggcatca tcagctgggg cgagggtgt gccgagcgca 761

acaggccccg ggtctacatc agcctctctg cgcaccgctc ctgggtggag aagatcgtgc 821

15

aaggggtgca gctccgcggg cgcgctcagg ggggtggggc cctcaggga ccgagccagg 881

gctctggggc cgccgcgcgc tcctagggcg cagcgggacg cggggctcgg atctgaaagg 941

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aataggctca tctacctcta cctctggggg cccggacggc tgctgcggaa aggaaacccc 1061

ctccccgacc cgcccgacgg cctcaggccc cgccctccaa ggcatcaggc cccgcccac 1121

20

ggcctcatgt ccccgcccc aagacttccg gccccgcccc cgggccccag cgcttttgtg 1181

tatataaatg ttaatgattt ttataggtat ttgtaaccct gccacatat c 1232

<210> 8

<211> 146

25

<212> PRT

<213> human

<400> 8

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
 5 -45 -40 -35
 Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala
 -30 -25 -20
 Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val
 -15 -10 -5 -1 1
 10 Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile
 5 10 15
 Gln Lys Asn Gly Thr His His Cys Ala Gly Gln Pro Glu Gln Thr Ile Pro
 20 25 30 35
 Val Leu Cys Ala Ala Gly Gly Leu Ala Ala Gly Glu Pro Trp Leu Ser Val
 15 40 45 50
 Pro Glu Gly Gly Cys Cys Leu Gly Gly Ala Pro Pro Cys Val Phe Leu Glu
 55 60 65
 Gly Arg Cys Leu Cys Arg His Cys Pro Gly Ala Ser Arg Ala Leu His Thr
 70 75 80 85
 20 Val Leu Arg Ala Gly Pro Ala His Leu Pro Thr
 90 95

<210> 9

<211> 952

25 <212> DNA

<213> human

<400> 9

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gcc atg gtg gtt tct gga gcg ccc cca gcc ctg ggt ggg ggc tgt ctc ggc  51
5      Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

          -45          -40          -35

acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat gcg gcc 102
      Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

          -30          -25          -20

10     agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt 153
      Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

          -15          -10          -5          -1  1

      gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg atc gtg agc atc 204
      Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

15              5              10              15

      cag aag aat ggg acc cac cac tgc gca gtt ccc ttg ccc cac cct cag acc 255
      Gln Lys Asn Gly Thr His His Cys Ala Val Pro Leu Pro His Pro Gln Thr

          20          25          30          35

      ctg cag aag ctg aag gtt cct atc atc gac tcg gaa gtc tgc agc cat ctg 306
20     Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His Leu

          40          45          50

      tac tgg cgg gga gca gga cag gga ccc atc act gag gac atg ctg tgt gcc 357
      Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met Leu Cys Ala

          55          60          65

25     ggc tac ttg gag ggg gag cgg gat gct tgt ctg ggc gac tcc ggg ggc ccc 408

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Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly Asp Ser Gly Gly Pro
 70 75 80 85
 ctc atg tgc cag gtg gac ggc gcc tgg ctg ctg gcc ggc atc atc agc tgg 459
 Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu Ala Gly Ile Ile Ser Trp
 5 90 95 100
 ggc gag ggc tgt gcc gag cgc aac agg ccc ggg gtc tac atc agc ctc tct 510
 Gly Glu Gly Cys Ala Glu Arg Asn Arg Pro Gly Val Tyr Ile Ser Leu Ser
 105 110 115 120
 gcg cac cgc tcc tgg gtg gag aag atc gtg caa ggg gtg cag ctc cgc ggg 561
 10 Ala His Arg Ser Trp Val Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly
 125 130 135
 cgc gct cag ggg ggt ggg gcc ctc agg gca ccg agc cag ggc tct ggg gcc 612
 Arg Ala Gln Gly Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala
 140 145 150
 15 gcc gcg cgc tcc tagggcgcag cgggacgcgg ggctcggatc tgaaaggcgg 664
 Ala Ala Arg Ser
 155
 ccagatccac atctggatct ggatctgcgg cggcctcggg cggtttcccc cgccgtaaat 724
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 20 ccgacccgc ccgacggcct caggccccgc cctccaaggc atcaggcccc gcccaacggc 844
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 ataaatgtta atgattttta taggtatttg taacctgcc cacatatc 952
 <210> 10
 25 <211> 207

<212> PRT

<213> human

<400> 10

5 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
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 Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala
 -30 -25 -20
 Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val
 10 -15 -10 -5 -1 1
 Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile
 5 10 15
 Gln Lys Asn Gly Thr His His Cys Ala Val Pro Leu Pro His Pro Gln Thr
 20 25 30 35
 15 Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His Leu
 40 45 50
 Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met Leu Cys Ala
 55 60 65
 Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly Asp Ser Gly Gly Pro
 20 70 75 80 85
 Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu Ala Gly Ile Ile Ser Trp
 90 95 100
 Gly Glu Gly Cys Ala Glu Arg Asn Arg Pro Gly Val Tyr Ile Ser Leu Ser
 105 110 115 120
 25 Ala His Arg Ser Trp Val Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly

21

125

130

135

Arg Ala Gln Gly Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala

140

145

150

Ala Ala Arg Ser

5 155

<210> 11

<211> 1083

<212> DNA

10 <213> human

<400> 11

gcc atg gtg gtt tct gga gcg ccc cca gcc ctg ggt ggg ggc tgt ctc gcc 51

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

15 -45 -40 -35

acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat gcg gcc 102

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30 -25 -20

agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt 153

20 Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

-15 -10 -5 -1 1

gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg atc gtg agc atc 204

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

5 10 15

25 cag aag aat ggg acc cac cac tgc gca ggt tct ctg ctc acc agc cgc tgg 255

Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp
 20 25 30 35
 gtg atc act gct gcc cac tgt ttc aag gac aac ctg aac aaa cca tac ctg 306
 Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu
 5 40 45 50
 ttc tct gtg ctg ctg ggg gcc tgg cag ctg ggg aac cct ggc tct cgg tcc 357
 Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser
 55 60 65
 cag aag ttc cct tgc ccc acc ctc aga ccc tgc aga agc tgaaggttcc 406
 10 Gln Lys Phe Pro Cys Pro Thr Leu Arg Pro Cys Arg Ser
 70 75 80
 tatcatcgac tcggaagtct gcagccatct gtactggcgg ggagcaggac agggacccat 466
 cactgaggac atgctgtgtg ccggctactt ggagggggag cgggatgctt gtctgggcga 526
 ctccgggggc cccctcatgt gccaggtgga cggcgcctgg ctgctggccg gcatcatcag 586
 15 ctggggcgag ggctgtgccg agcgcaacag gcccggggtc tacatcagcc tctctgcgca 646
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 tggggccctc agggcaccga gccagggctc tggggccgcc gcgcgctcct agggcgccagc 766
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 20 gacggctgct gcggaaagga aacccccctc ccgaccggcc cgacggcctc agggccccgcc 946
 ctccaaggca tcaggccccg cccaacggcc tcatgtcccc gccccacga cttccggccc 1006
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 aacctgccc acatata 1083

23

<211> 131

<212> PRT

<213> human

5 <400> 12

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

-45

-40

-35

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30

-25

-20

10 Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

-15

-10

-5

-1 1

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

5

10

15

Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp

15 20 25 30 35

Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu

40

45

50

Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser

55

60

65

20 Gln Lys Phe Pro Cys Pro Thr Leu Arg Pro Cys Arg Ser

70

75

80

<210> 13

<211> 723

25 <212> DNA

<213> human

<400> 13

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gcc atg gtg gtt tct gga gcg ccc cca gcc ctg ggt ggg ggc tgt ctc gcc  51
5      Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
          -45          -40          -35

acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat gcg gcc  102
      Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala
          -30          -25          -20

10     agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt  153
      Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val
          -15          -10          -5          -1   1

      gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg atc gtg agc atc  204
      Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

15           5           10           15

      cag aag aat ggg acc cac cac tgc gca ggt tct ctg ctc acc agc cgc tgg  255
      Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp
          20           25           30           35

      gtg atc act gct gcc cac tgt ttc aag gac aac ctg aac aaa cca tac ctg  306
20     Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu
          40           45           50

      ttc tct gtg ctg ctg ggg gcc tgg cag ctg ggg aac cct ggc tct cgg tcc  357
      Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser
          55           60           65

25     cag aag gtg ggt gtt gcc tgg gtg gag ccc cac cct gtg tat tcc tgg aag  408

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25

Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys

70 75 80 85

gaa ggt gcc tgt gca gac att gcc ctg gtg cgt ctc gag cgc tcc ata cag 459

Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln

5 90 95 100

ttc tca gag cgg gtc ctg ccc atc tgc cta cct gat gcc tct atc cac ctc 510

Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu

105 110 115 120

cct cca aac acc cac tgc tgg atc tca ggc tgg ggg agc atc caa gat gga 561

10 Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly

125 130 135

gtt ccc ttg ccc cac cct cag acc ctc tcc aag gca tca ggc ccc gcc caa 612

Val Pro Leu Pro His Pro Gln Thr Leu Ser Lys Ala Ser Gly Pro Ala Gln

140 145 150

15 cgg cct cat gtc ccc gcc ccc acg act tcc ggc ccc gcc ccg ggc ccc agc 663

Arg Pro His Val Pro Ala Pro Thr Thr Ser Gly Pro Ala Pro Gly Pro Ser

155 160 165 170

gct ttt gtg tat ata aat gtt aat gat ttt tat agg tat ttg taaccctgcc 715

Ala Phe Val Tyr Ile Asn Val Asn Asp Phe Tyr Arg Tyr Leu

20 175 180 185

cacatatc

723

<210> 14

<211> 234

25 <212> PRT

〈213〉 human

<400> 14

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

5 -45 -40 -35

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30 -25 -20

Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

-15 -10 -5 -1 1

10 Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

5 10 15

Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp

20 25 30 35

Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu

15 40 45 50

Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser

55 60 65

Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys

70 75 80 85

20 Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln

90 95 100

Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu

105 110 115 120

Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly

25 125 130 135

27

Val Pro Leu Pro His Pro Gln Thr Leu Ser Lys Ala Ser Gly Pro Ala Gln

140

145

150

Arg Pro His Val Pro Ala Pro Thr Thr Ser Gly Pro Ala Pro Gly Pro Ser

155

160

165

170

5 Ala Phe Val Tyr Ile Asn Val Asn Asp Phe Tyr Arg Tyr Leu

175

180

185

<210> 15

<211> 1004

10 <212> DNA

<213> human

<400> 15

gcc atg gtg gtt tct gga gcg ccc cca gcc ctg ggt ggg ggc tgt ctc ggc 51

15 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

-45

-40

-35

acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat gcg gcc 102

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30

-25

-20

20 agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt 153

Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

-15

-10

-5

-1 1

gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg atc gtg agc atc 204

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

25

5

10

15

cag aag aat ggg acc cac cac tgc gca ggt tct ctg ctc acc agc cgc tgg 255
 Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp
 20 25 30 35
 gtg atc act gct gcc cac tgt ttc aag gat tcc ctt gcc cca ccc tca gac 306
 5 Val Ile Thr Ala Ala His Cys Phe Lys Asp Ser Leu Ala Pro Pro Ser Asp
 40 45 50
 cct gca gaa gct gaa ggt tcc tat cat cga ctc gga agt ctg cag cca tct 357
 Pro Ala Glu Ala Glu Gly Ser Tyr His Arg Leu Gly Ser Leu Gln Pro Ser
 55 60 65
 10 gta ctg gcg ggg agc agg aca ggg acc cat cac tgaggacatg ctgtgtgccg 410
 Val Leu Ala Gly Ser Arg Thr Gly Thr His His
 70 75 80
 gctacttga gggggagcgg gatgcttgtc tgggcgactc cgggggcccc ctcatgtgcc 470
 aggtggacgg cgcttgctg ctggccggca tcatcagctg gggcgagggc tgtgccgagc 530
 15 gcaacaggcc cggggtctac atcagcctct ctgcgcaccg ctcctgggtg gagaagatcg 590
 tgcaaggggt gcagctccgc gggcgcgctc aggggggtgg ggccctcagg gcaccgagcc 650
 agggctcttg ggccgccg cgctcctagg gcgcagcggg acgcggggct cggatctgaa 710
 aggcggccag atccacatct ggatctggat ctgcggcggc ctcgggcggg ttccccgcc 770
 gtaaataggc tcatctacct ctacctctgg gggcccggac ggctgctgcg gaaaggaaac 830
 20 cccctccccg acccgcccga cggcctcagg ccccgccctc caaggcatca ggccccgcc 890
 aacggcctca tgtccccgc cccacgactt ccggccccgc ccccgggccc cagcgctttt 950
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<210> 16

25 <211> 129

29

<212> PRT

<213> human

<400> 16

5 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
 -45 -40 -35
 Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala
 -30 -25 -20
 Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val
 10 -15 -10 -5 -1 1
 Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile
 5 10 15
 Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp
 20 25 30 35
 15 Val Ile Thr Ala Ala His Cys Phe Lys Asp Ser Leu Ala Pro Pro Ser Asp
 40 45 50
 Pro Ala Glu Ala Glu Gly Ser Tyr His Arg Leu Gly Ser Leu Gln Pro Ser
 55 60 65
 Val Leu Ala Gly Ser Arg Thr Gly Thr His His
 20 70 75 80

<210> 17

<211> 948

<212> DNA

25 <213> human

<400> 17

gcc atg gtg gtt tct gga gcg ccc cca gcc ctg ggt ggg ggc tgt ctc gcc 51

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

5 -45 -40 -35

acc ttc acc tcc ctg ctg ctg ctg gcg tcg aca gcc atc ctc aat gcg gcc 102

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30 -25 -20

agg ata cct gtt ccc cca gcc tgt ggg aag ccc cag cag ctg aac cgg gtt 153

10 Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

-15 -10 -5 -1 1

gtg ggc ggc gag gac agc act gac agc gag tgg ccc tgg atc gtg agc atc 204

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

5 10 15

15 cag aag aat ggg acc cac cac tgc gca ggt tct ctg ctc acc agc cgc tgg 255

Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp

20 25 30 35

gtg atc act gct gcc cac tgt ttc aag gac aac ctg aac aaa cca tac ctg 306

Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu

20 40 45 50

ttc tct gtg ctg ctg ggg gcc tgg cag ctg ggg aac cct ggc tct cgg tcc 357

Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser

55 60 65

cag aaa gtg ggt gtt gcc tgg gtg gag ccc cac cct gtg tat tcc tgg aag 408

25 Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys

31

	70	75	80	85	
	gaa ggt gcc tgt gca gac att gcc ctg gtg cgt ctc gag cgc tcc ata cag				459
	Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln				
	90	95	100		
5	ttc tca gag cgg gtc ctg ccc atc tgc cta cct gat gcc tct atc cac ctc				510
	Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu				
	105	110	115	120	
	cct cca aac acc cac tgc tgg atc tca ggc tgg ggg agc atc caa gat gga				561
	Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly				
10	125	130	135		
	gtt ccc ttg ccc cac cct cag acc ctg cag aag ctg aag gtt cct atc atc				612
	Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile				
	140	145	150		
	gac tcg gaa gtc tgc agc cat ctg tac tgg cgg gga gca gga cag gga ccc				663
15	Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro				
	155	160	165	170	
	atc act gag gac atg ctg tgt gcc ggc tac ttg gag ggg gag cgg gat gct				714
	Ile Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala				
	175	180	185		
20	tgt ctg gtg agc tcc ctc gag ccc ccc acc cct ggc cag gag ggc ctc ggg				765
	Cys Leu Val Ser Ser Leu Glu Pro Pro Thr Pro Gly Gln Glu Gly Leu Gly				
	190	195	200	205	
	aag gag cca gcg tca gtc ctg tcc cca ctg agc ccc aca acc tct ccc tgg				816
	Lys Glu Pro Ala Ser Val Leu Ser Pro Leu Ser Pro Thr Thr Ser Pro Trp				
25	210	215	220		

32

cct cct ccc cag aac tgg ctg tgc ctg aca gtc ccg ggt ccc cat aga acc 867

Pro Pro Pro Gln Asn Trp Leu Cys Leu Thr Val Pro Gly Pro His Arg Thr

225

230

235

agc ctc agc ctg gct cag cca ctc act tat ttg ttc aga cat taaactgggc 919

5

Ser Leu Ser Leu Ala Gln Pro Leu Thr Tyr Leu Phe Arg His

240

245

250

atcccagctg caaaaaaaaa aaaaaaaaaa

948

<210> 18

10

<211> 302

<212> PRT

<213> human

<400> 18

15

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly

-45

-40

-35

Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala

-30

-25

-20

Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val

20

-15

-10

-5

-1 1

Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile

5

10

15

Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp

20

25

30

35

25

Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu

	40	45	50
	Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser		
	55	60	65
	Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys		
5	70	75	80 85
	Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln		
	90	95	100
	Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu		
	105	110	115 120
10	Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly		
	125	130	135
	Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile		
	140	145	150
	Asp Ser Glu Val Cys Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro		
15	155	160	165 170
	Ile Thr Glu Asp Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala		
	175	180	185
	Cys Leu Val Ser Ser Leu Glu Pro Pro Thr Pro Gly Gln Glu Gly Leu Gly		
	190	195	200 205
20	Lys Glu Pro Ala Ser Val Leu Ser Pro Leu Ser Pro Thr Thr Ser Pro Trp		
	210	215	220
	Pro Pro Pro Gln Asn Trp Leu Cys Leu Thr Val Pro Gly Pro His Arg Thr		
	225	230	235
	Ser Leu Ser Leu Ala Gln Pro Leu Thr Tyr Leu Phe Arg His		
25	240	245	250

<210> 19

<211> 1322

<212> DNA

5 <213> mouse

<400> 19

cctgccagtc tcaagcaaca cagcccttag gtcctttgag ccggccagca gccttgctgg 60

gtctccaccc ataccagca atg atg atc tcc aga cct ccc cca gca ctg ggt 112

10 Met Met Ile Ser Arg Pro Pro Pro Ala Leu Gly

-45

-40

ggg gac cag ttc agc atc tta atc ctt ctg gtg ctg ctg act tcc aca gct 163

Gly Asp Gln Phe Ser Ile Leu Ile Leu Leu Val Leu Leu Thr Ser Thr Ala

-35

-30

-25

15 ccc atc agt gct gcc acc atc cga gtg tcc cca gac tgt ggg aag cct cag 214

Pro Ile Ser Ala Ala Thr Ile Arg Val Ser Pro Asp Cys Gly Lys Pro Gln

-20

-15

-10

-5

cag ctg aac cgg att gtg gga ggt gag gac agc atg gat gcc cag tgg ccc 265

Gln Leu Asn Arg Ile Val Gly Gly Glu Asp Ser Met Asp Ala Gln Trp Pro

20 -1 1 5 10

tgg att gtt agc atc ctc aag aat ggc tcc cac cac tgt gca ggc tcc ctg 316

Trp Ile Val Ser Ile Leu Lys Asn Gly Ser His His Cys Ala Gly Ser Leu

15

20

25

30

ctc acc aac cgc tgg gtg gtc aca gcc gcg cac tgc ttt aag agc aat atg 367

25 Leu Thr Asn Arg Trp Val Val Thr Ala Ala His Cys Phe Lys Ser Asn Met

35

	35	40	45	
	gac aaa cca tct ctg ttc tca gta ttg ttg ggg gcc tgg aag ctg ggg agc			418
	Asp Lys Pro Ser Leu Phe Ser Val Leu Leu Gly Ala Trp Lys Leu Gly Ser			
	50	55	60	
5	cca ggc cca agg tcc cag aaa gta ggc att gct tgg gtg ctg cct cac ccc			469
	Pro Gly Pro Arg Ser Gln Lys Val Gly Ile Ala Trp Val Leu Pro His Pro			
	65	70	75	80
	agg tat tct tgg aag gag gga acc cat gca gac att gcc ctg gtg cgc ctg			520
	Arg Tyr Ser Trp Lys Glu Gly Thr His Ala Asp Ile Ala Leu Val Arg Leu			
10	85	90	95	
	gaa cac tcc atc cag ttc tct gag cgg atc ctg ccc atc tgc cta cct gac			571
	Glu His Ser Ile Gln Phe Ser Glu Arg Ile Leu Pro Ile Cys Leu Pro Asp			
	100	105	110	115
	tcc tct gtc cgt ctc cct ccc aag acc gac tgc tgg att gcc ggc tgg gga			622
15	Ser Ser Val Arg Leu Pro Pro Lys Thr Asp Cys Trp Ile Ala Gly Trp Gly			
	120	125	130	
	agc atc cag gat gga gtg ccc ctg ccc cac cct cag acc ctt cag aag ctg			673
	Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu			
	135	140	145	
20	aag gtg ccc atc atc gac tcc gaa ctc tgc aaa agc ttg tac tgg cgg gga			724
	Lys Val Pro Ile Ile Asp Ser Glu Leu Cys Lys Ser Leu Tyr Trp Arg Gly			
	150	155	160	165
	gcc ggt cag gaa gcc atc acg gag ggc atg ctg tgt gct ggt tac ctg gaa			775
	Ala Gly Gln Glu Ala Ile Thr Glu Gly Met Leu Cys Ala Gly Tyr Leu Glu			
25	170	175	180	

ggg gag cgg gat gct tgt ctg ggc gac tct ggg ggt ccc ctg atg tgc cag 826
 Gly Glu Arg Asp Ala Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln
 185 190 195 200
 gtg gat gac cac tgg cta ctg act ggc ata atc agc tgg gga gag ggc tgc 877
 5 Val Asp Asp His Trp Leu Leu Thr Gly Ile Ile Ser Trp Gly Glu Gly Cys
 205 210 215
 gga gcg caa ccg gcc cgg tgt gta cac cag cct cct agc tca ccg ctc ctg 928
 Gly Ala Gln Pro Ala Arg Cys Val His Gln Pro Pro Ser Ser Pro Leu Leu
 220 225 230
 10 ggt gca aag gat cgt tca agg ggt gca gct gcg cgg gta ctt ggc gga cag 979
 Gly Ala Lys Asp Arg Ser Arg Gly Ala Ala Ala Arg Val Leu Gly Gly Gln
 235 240 245 250
 tgg gga cac agg aag ctc cta atc taggatctga agatgagcag cctcctgcaa 1033
 Trp Gly His Arg Lys Leu Leu Ile
 15 255
 ttctctctgc tgtaaataatg tcttctacct ccggggggcg cccgcggcct gagcgagaga 1093
 acaaggaagt tctggaaccg cccacataga ggatccgccc ctcaatcgag gactctgtgt 1153
 gtgtgtgtgt gtgtgtgtgt gtgtgtgcct ctgtgtgcgt gtgtatgcgc gcgcacgtgc 1213
 gcgcgagagc aatgatTTTT ttttttacag ttatacgtaa ccatgcccac atatttattc 1273
 20 cagtttcaat aaattattta ttcttaaaaa aaaaaaaaaa aaaaaaaaaa 1322

<210> 20

<211> 308

<212> PRT

25 <213> mouse

<400> 20

Met Met Ile Ser Arg Pro Pro Pro Ala Leu Gly

-45

-40

5 Gly Asp Gln Phe Ser Ile Leu Ile Leu Leu Val Leu Leu Thr Ser Thr Ala

-35

-30

-25

Pro Ile Ser Ala Ala Thr Ile Arg Val Ser Pro Asp Cys Gly Lys Pro Gln

-20

-15

-10

-5

Gln Leu Asn Arg Ile Val Gly Gly Glu Asp Ser Met Asp Ala Gln Trp Pro

10

-1 1

5

10

Trp Ile Val Ser Ile Leu Lys Asn Gly Ser His His Cys Ala Gly Ser Leu

15

20

25

30

Leu Thr Asn Arg Trp Val Val Thr Ala Ala His Cys Phe Lys Ser Asn Met

35

40

45

15 Asp Lys Pro Ser Leu Phe Ser Val Leu Leu Gly Ala Trp Lys Leu Gly Ser

50

55

60

Pro Gly Pro Arg Ser Gln Lys Val Gly Ile Ala Trp Val Leu Pro His Pro

65

70

75

80

Arg Tyr Ser Trp Lys Glu Gly Thr His Ala Asp Ile Ala Leu Val Arg Leu

20

85

90

95

Glu His Ser Ile Gln Phe Ser Glu Arg Ile Leu Pro Ile Cys Leu Pro Asp

100

105

110

115

Ser Ser Val Arg Leu Pro Pro Lys Thr Asp Cys Trp Ile Ala Gly Trp Gly

120

125

130

25 Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu Gln Lys Leu

38

135 140 145
 Lys Val Pro Ile Ile Asp Ser Glu Leu Cys Lys Ser Leu Tyr Trp Arg Gly
 150 155 160 165
 Ala Gly Gln Glu Ala Ile Thr Glu Gly Met Leu Cys Ala Gly Tyr Leu Glu
 5 170 175 180
 Gly Glu Arg Asp Ala Cys Leu Gly Asp Ser Gly Gly Pro Leu Met Cys Gln
 185 190 195 200
 Val Asp Asp His Trp Leu Leu Thr Gly Ile Ile Ser Trp Gly Glu Gly Cys
 205 210 215
 10 Gly Ala Gln Pro Ala Arg Cys Val His Gln Pro Pro Ser Ser Pro Leu Leu
 220 225 230
 Gly Ala Lys Asp Arg Ser Arg Gly Ala Ala Ala Arg Val Leu Gly Gly Gln
 235 240 245 250
 Trp Gly His Arg Lys Leu Leu Ile
 15 255

 <210> 21
 <211> 99
 <212> DNA
 20 <213> Artificial Sequence
 <220>
 <223> Designed oligonucleotide to construct plasmid pSecTrypHis

 <400> 21
 25 aagcttggct agcaacacca tgaatctact cctgatcctt acctttgttg ctgctgctgt 60

tgctgcccc tttgacgacg atgacaagga tccgaattc

99

<210> 22

<211> 99

5 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

10 <400> 22

gaattcggat ccttgatc gtcgtcaaag ggggcagcaa cagcagcagc aacaaaggta 60

aggatcagga gtagattcat ggtgttgcta gccaaagctt

99

<210> 23

15 <211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

20

<400> 23

ttggtgcatg gcgga

15

<210> 24

25 <211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

5

<400> 24

tcctcgagac ttggcctgaa tggtttt

27

<210> 25

10

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid

15

pSecTrypHis/Neurosin

<400> 25

gcgctagcag atctccatga atctactcct gatcc

35

20

<210> 26

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

25

<223> Designed oligonucleotide primer to amplify a portion of plasmid

pSecTrypHis/Neurosin

<400> 26

tgaagcttgc catggaccaa cttgtcatc

29

5

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pTrypHis

<400> 27

ccaagcttca ccatcaccat caccat

26

15

<210> 28

<211> 17

<212> DNA

<213> Artificial Sequence

20

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid
pTrypSigTag

<400> 28

25

gcacagtcga ggctgat

17

<210> 29

<211> 17

<212> DNA

5 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid
pFBTrypSigTag

10 <400> 29

caaatgtggt atggctg

17

<210> 30

<211> 20

15 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify conserved region of serin
proteases-encoding sequence

20 <220>

<221> UNSURE

<222> 9, 12

<223> n is a, c, g or t.

25 <400> 30

gtgctcacng cngcbcaytg

20

<210> 31

<211> 20

5 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify conserved region of serin
proteases-encoding sequence

10 <220>

<221> UNSURE

<222> 12, 15

<223> n is a, c, g or t.

15 <400> 31

ccvctrwsdc cncnggcga

20

<210> 32

<211> 20

20 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP4F1 for RACE for human
BSSP4 (forward)

25

<400> 32

aggttcctat catcgactcg

20

<210> 33

5 <211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP4F2 for RACE for human

10 BSSP4 (forward)

<400> 33

tgaggacatg ctgtgtgccg g

21

15 <210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

20 <223> Designed oligonucleotide primer designated as hBSSP4F3 to amplify mature
human BSSP4-encoding region (forward)

<400> 34

gttgtgggcg gcgaggacag

20

25

45

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

5 <220>

<223> Designed oligonucleotide primer designated as hBSSP4F6 to amplify full-length human BSSP4-encoding mRNA (forward)

<400> 35

10 gccatggtgg tttctggagc

20

<210> 36

<211> 21

<212> DNA

15 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP4R1 for RACE for human BSSP4 (reverse)

20 <400> 36

tatggtttgt tcaggttgtc c

21

<210> 37

<211> 20

25 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP4R2 for RACE for human
BSSP4 (reverse)

5

<400> 37

agggcaatgt ctgcacaggc

20

<210> 38

10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

15

<223> Designed oligonucleotide primer designated as hBSSP4R3/E to amplify full-
length human BSSP4-encoding mRNA (reverse)

<400> 38

ctgaattcct aggagcgcgc ggcggcc

27

20

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

25

<223> Designed oligonucleotide primer designated as hBSSP4R4/E to amplify full-

length human BSSP4-encoding mRNA (reverse)

<400> 39

gagaattcga tatgtgggca gggttaca

28

5

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Designed oligonucleotide primer designated as mBSSP4.1 for RACE for mouse
BSSP4 (forward)

<400> 40

15

acaaaccatc tctgttctca g

21

<210> 41

<211> 20

<212> DNA

20

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP4F2 for RACE for mouse
BSSP4 (forward)

25

<400> 41

gtcccagaaa gtaggcattg

20

<210> 42

<211> 20

5 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP4F3 to amplify full-length mouse BSSP4-encoding mRNA (forward)

10

<400> 42

ctccacccat accagcaatg

20

<210> 43

15 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP4F4 to amplify mature mouse BSSP4-encoding region (forward)

20

<400> 43

attgtgggag gtgaggacag

20

25 <210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Designed oligonucleotide primer designated as mBSSP4.2 for RACE for mouse
BSSP4 (reverse)

<400> 44

tgccagagttc ggagtcgatg

20

10

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Designed oligonucleotide primer designated as mBSSP4R2 for RACE for mouse
BSSP4 (reverse)

<400> 45

20 atccagcagt cggctcttggg

20

<210> 46

<211> 30

<212> DNA

25 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP4R3/P to amplify full-length mouse BSSP4-encoding mRNA (reverse)

5 <400> 46

attctgcagt tccttgttct ctcgctcagg

30

<210> 47

<211> 117

10 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

15 <400> 47

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TGCTGCCCCC TTTCACCATC ACCATCACCA TGACGACGAT GACAAGGATC CGAATTC 117

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20 <211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

25

<400> 48

GAATTCGGAT CCTTGCATC GTCGTCATGG TGATGGTGAT GGTGAAAGGG GGCAGCAACA 60

GCAGCAGCAA CAAAGGTAAG GATCAGGAGT AGATTCATGG TGTGCTAGC CAAGCTT 117

5

10